

Supplementary Information

Phylogenomic Perspective on a Unique *Mycobacterium bovis* Clade Dominating Bovine Tuberculosis Infections among Cattle and Buffalos in Northern Brazil

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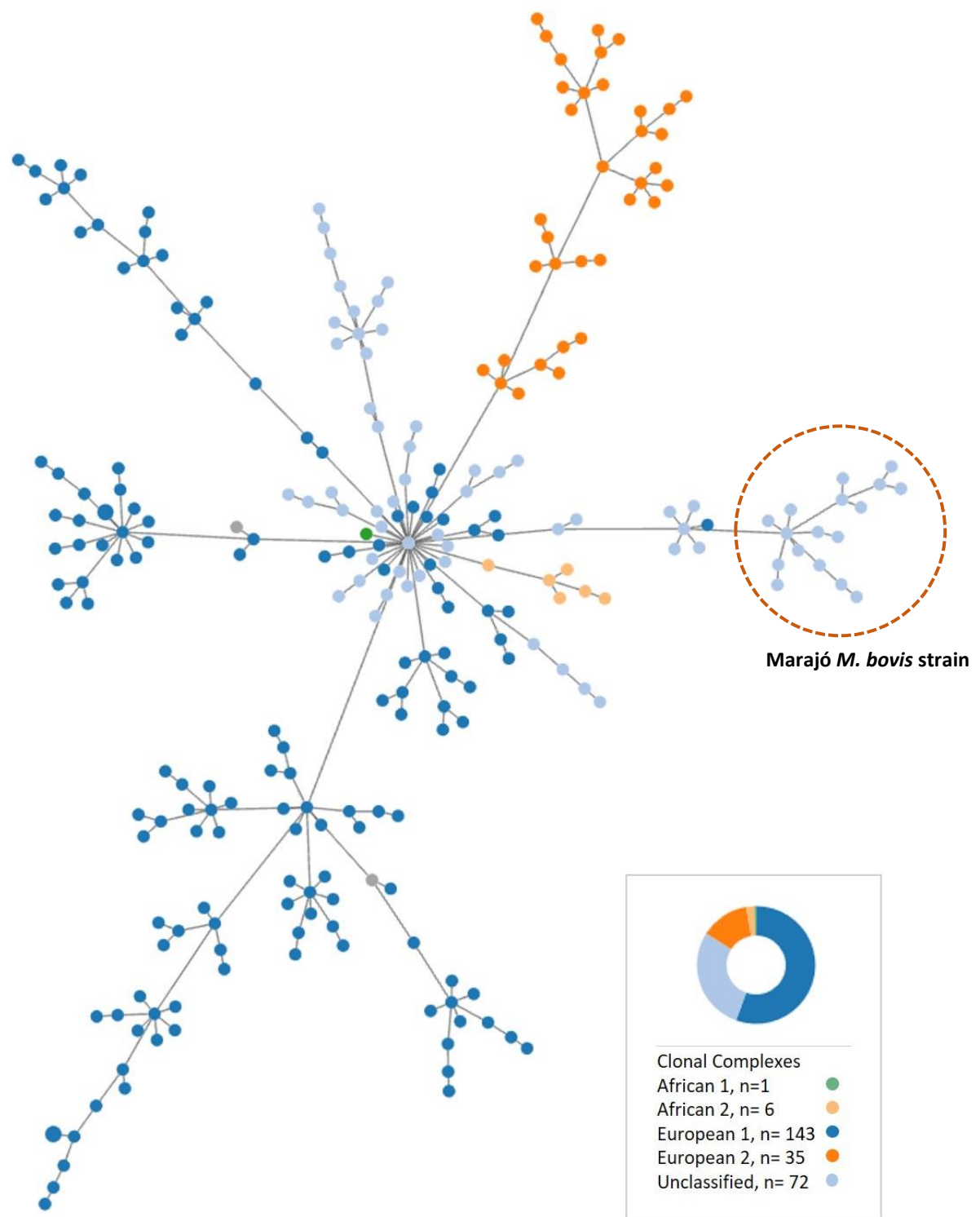
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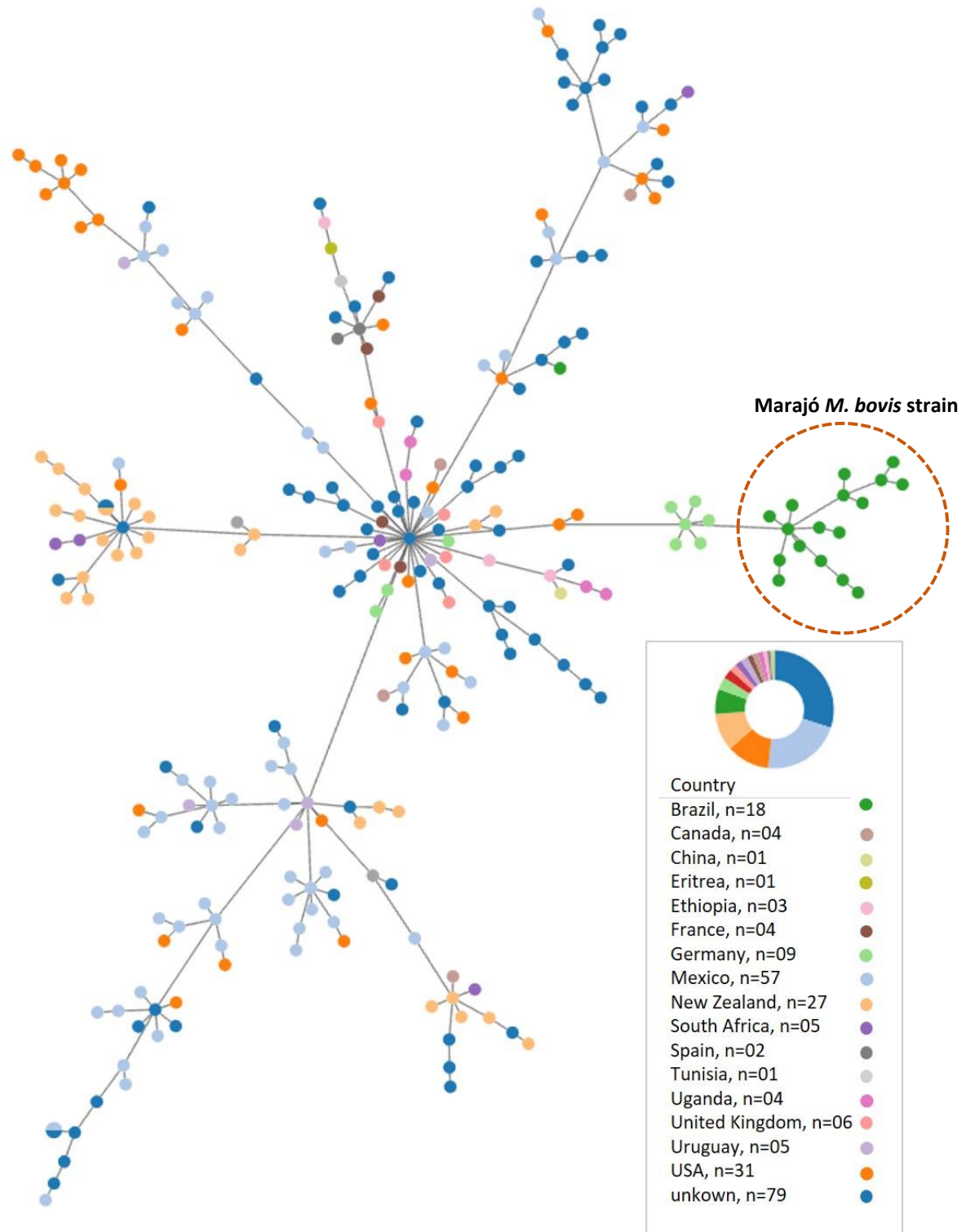
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Supplementary Figure S1 – Minimum Spanning Tree of 257 *M. bovis* isolates, including 17 *M. bovis* isolated from buffalos and cattle in the Marajó Island. The Minimum Spanning Tree was constructed with the goeBURST algorithm using the pairwise distance method as implemented in Phyloviz (<http://online2.phyloviz.net/index>) and based on 20 103 SNPs. Nodes are coloured by Clonal Complex. Both European 2 and African 2 isolates comprise distinct monophyletic branches, contrarily to the European 1, which, using this algorithm does not form a single monophyletic subtree. The Marajó strains are highlighted on the tree forming a separate branch.



Supplementary Figure S2 – Minimum Spanning Tree of 257 *M. bovis* isolates, including 17 *M. bovis* isolated from buffalos and cattle in the Marajó Island. The Minimum Spanning Tree was constructed with the goeBURST algorithm using the pairwise distance method as implemented in Phyloviz (<http://online2.phyloviz.net/index>) and based on 20 103 SNPs. Nodes are coloured by country of isolation. The Marajó strains are highlighted on the tree forming a separate branch, distancing at least 79 SNPs from the nearest *M. bovis* isolate (Germany)